

*Fig. 1*

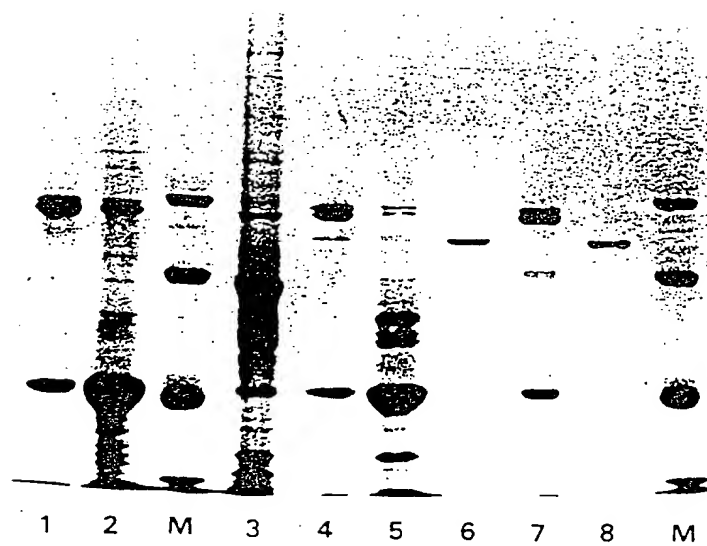


Fig. 2

adseverin C39	KVAHVKQIPFDA
gelsolin	<sup>386</sup> HIANVERVPFDA
villin	<sup>365</sup> KVAKVEQVKFDA

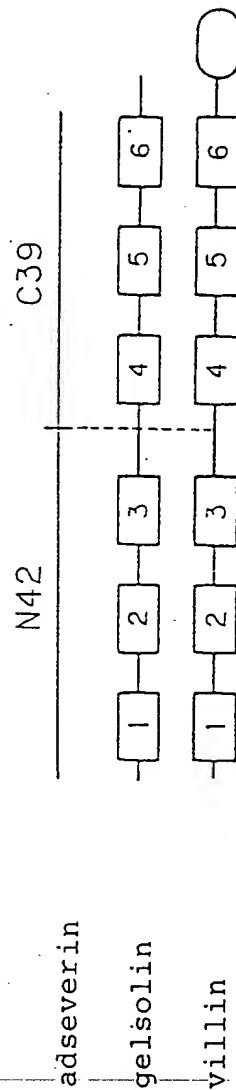


Fig. 3

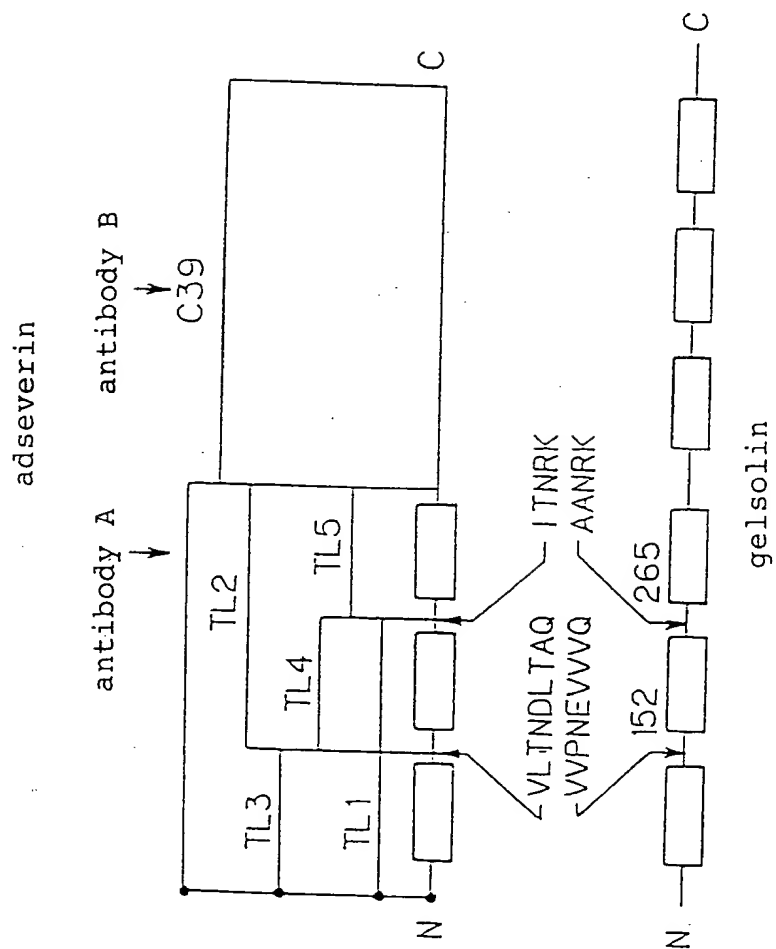


Fig. 4

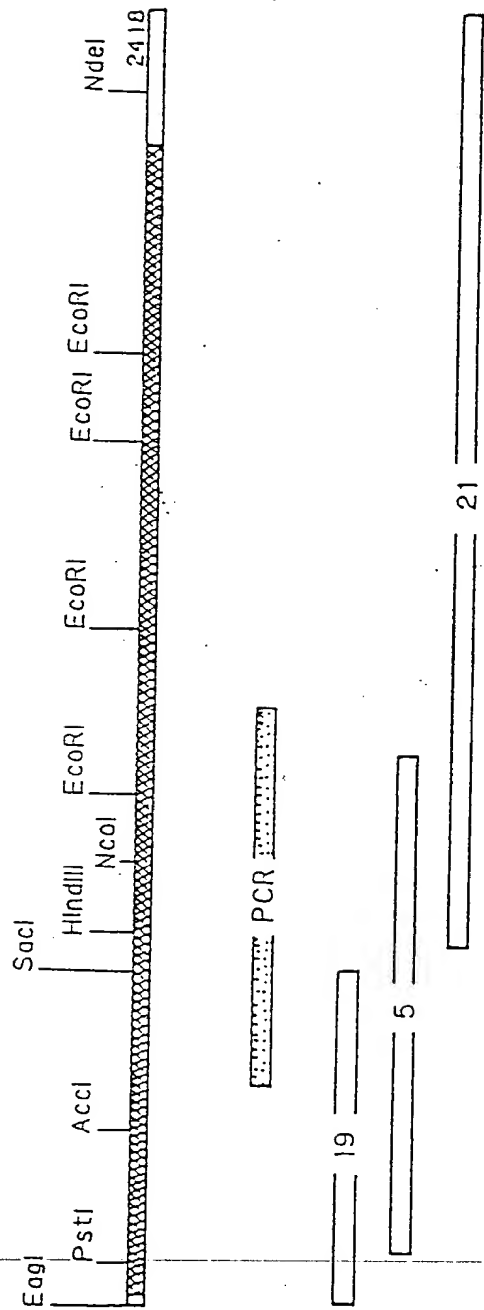


Fig. 5A

ADS	008	EEFAR-AGK-R	AGLQVWRIE	KLEIVPVPE	SAYGN	1
GEL	057	PEFLK-AGK-E	PGLQIWRIE	KEDLVVP	PTNL YGD	
VIL	007	QVKGS-INITT	PGLQIWRIE	AMQMPVP	SPSSTFGS	
ADS	385	AAQHHVVDDGS	GKVQIWRIE	NGRVEI	DRNSYGE	
GEL	434	AAQHGMDDDGT	GQKQIWRIE	GSNKVP	VDPATY GQ	4
VIL	387	AAQQKMVDDGS	GEVQVWRIE	NLELV	PVDSKWLGH	
ADS	127	NHVLTNDLTAQ	RLLHVKGRR	-VVRATE	EVPLSWDS	
GEL	177	KHVPNEVVVQ	RLFQVKGR	-VVRATE	VPVSWES	2
VIL	127	KHVEITNSYDVQ	RLLHVKGKR	NVV-AGE	VEMSWKS	
ADS	503	GQAPAPI--RL	FQVRRNLAS	ITRIM-	EVDDV DANS	
GEL	556	GQTAFAST--RL	FQVRANSAG	ATRAV-	EVLPRKAGA	5
VIL	508	NLETGPST--RL	FQVQGTGAN	NTKAF-	EVPARANF	
ADS	245	NRKMAK-LYMV	SDASGSMKV	SLVAEEN	PFSMAM	
GEL	294	NRKLAK-LYKV	SNGAGTMSV	SLVADEN	PFAQGA	3
VIL	250	KAAL-K-LYHV	SDSEGNLVV	REVAT-	RPLTQDL	
ADS	610	ED-HPRLYGC	SNKTGRFII	EEVPGE--	FTQDD	
GEL	662	MDAHPRLFAC	SNKIGRFVI	EEVPGE--	LMQED	6
VIL	615	LVI-TPRLFEC	SNKTGRFLA	TEIP-D--	FNQDD	

Fig. 5B

ADS	F	YVG	D	A	YLV	LHTTQASRG---FTYR	L	HF	W	L	G	KECTQD	E	STA	A	1
GEL	F	FTG	D	A	YVI	LKTVQLRNGN--LQYD	L	HY	W	L	G	NECSQD	E	SGA	A	
VIL	F	FDG	D	C	YII	LAIH--KTASS-LSYD	I	HY	W	I	G	QDSSLD	E	QGA	A	
ADS	F	YGG	D	C	YII	LYTYPR---GQI---	I	YT	W	Q	G	ANATRD	E	LTT	S	4
GEL	F	YGG	D	S	YII	LYNYRHGGRQGI---	I	YN	W	Q	G	AQSTQD	E	VAA	S	
VIL	F	YGG	D	C	YLL	LYTYLIGEKQHYL---	L	YV	W	Q	G	SQASQD	E	ITA	S	
ADS	F	NKG	D	C	FII	-----DLGTE	I	YQ	W	C	G	SSCNKY	E	RLK	A	2
GEL	F	NNG	D	C	FIL	-----DLGNN	I	HQ	W	C	G	SNSNRY	E	RLK	A	
VIL	F	NRG	D	V	FLL	-----DLGKL	I	IQ	W	N	G	PESTRM	E	RLR	G	
ADS	L	NSN	D	V	FVL	-----KLRQNN	G	YI	W	I	G	KGSTQE	E	EKG	A	5
GEL	L	NSN	D	A	FVL	-----KT-PSA	A	YL	W	V	G	TGASEA	E	KTG	A	
VIL	L	NSN	D	V	FVL	-----KT-QSC	C	YL	W	C	G	KGCSCD	E	REM	A	
ADS	L	LSE	E	C	FIL	-----DHGAQKQ	I	FV	W	K	G	KDANPQ	E	RKA	A	3
GEL	L	KSE	D	C	FIL	-----DHGKDGK	I	FV	W	K	G	KQANTE	E	RKA	A	
VIL	L	SHE	D	C	YIL	-----DQG-GLK	I	YV	W	K	G	KKANEQ	E	KKG	A	
ADS	L	AED	D	V	MLL	-----DAWEQ	I	FI	W	I	G	KDANEV	E	KSE	S	6
GEL	L	ATD	D	V	MLL	-----DTWDQ	V	FV	W	V	G	KDSQEE	E	KTE	A	
VIL	L	EED	D	V	FLL	-----DVWDQ	V	FF	W	I	G	KHANEV	E	KKA	A	

← Motif B →

← Motif A →

Fig. 5C

ADS	AIFTVQMDDYLGKPVQNRREL-----	QG	Y	ES	TD	FV	G	YF	1
GEL	AIFTVQLDYLNGRAVQHREV-----	QG	F	ES	AT	FL	G	YF	
VIL	AIYTTQMDDFLKGRAVQHREV-----	QG	N	ES	EA	FR	G	YF	
ADS	AFLTVQLDRSLGGQAVQIRVS-----	QG	K	EP	AH	LL	S	LF	4
GEL	AILTAQLDELGGTPVQSRVV-----	QG	K	EP	AH	LM	S	LF	
VIL	AYQAVILDQKYNGEPVQIRVP-----	MG	K	EP	PH	LM	S	IF	
ADS	SQVAIGIRDNERKGRAQLIVE-----	EG	S	EP	SE	LT	K	VL	2
GEL	TQVSKGIRDNERSGRARVHVSE----	EG	T	EP	EA	ML	Q	VL	
VIL	MTLAKEIRDQERGGRITYGVVDGEN	EL	A	SP	-K	LM	E	VM	
ADS	EYVASVL-----KCKTSTIQ-----	EG	K	EP	EE	FW	N	SL	5
GEL	QELLRLV-----RAQPVQVA-----	EG	S	EP	DG	FW	E	AL	
VIL	KMVADTISRTEK-----QV-VV-----	EG	Q	EP	AN	FW	M	AL	
ADS	MKTAEFFLQOMNYSNT-QIQVLP-	EG	G	ET	P	IF	KQ	FF	3
GEL	LKTASDFITKMDYPKQT-QVSVLP-	EG	G	ET	P	LF	KQ	FF	
VIL	MSHALNFIKAKQYPPST-QVEVQN-	DG	A	ES	A	VF	QQ	LF	
ADS	LKSAKIYLETDPGGRDKRTPIVIIL	QG	H	EP	PT	FT	GW	FL	6
GEL	LTSAKRYIETDPANRDRPTITVVK	QG	F	EP	PS	FV	GW	FL	
VIL	ATTAQOEYLKTHPSGRDPETPIIVK	QG	H	EP	PT	FT	GW	FL	

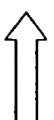
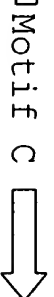
 Motif C 

Fig. 5D

ADS	- KGGLKY---KA	GGVASGL	126	
GEL	- KSGGLKY---KK	GGVASGF	176	1
VIL	- KQGLVI---RK	GGVASGM	126	
ADS	- ---KDKPLI IY	KNGTSKKE	502	
GEL	- ---GGKPMI IY	KGGSREG	555	4
VIL	- ---KGR-MV VY	QGGTSRTN	507	
ADS	- ---GEKPKLRD	GEDDDIKADIT	244	
GEL	- ---GPKPALPA	GTEDTA-KEDAA	293	2
VIL	N HVLGKRRELKA	AVPDTV-VEPAL	249	
ADS	- ---GGK---KD	YQTS-PLLESQA	609	
GEL	- ---GGK---AA	YRTS-PLKDKK	661	5
VIL	- ---GGK---AP	YANT-KRLQ EEN	614	
ADS	K DWRDRDQSDGF	GKVYVTEKVAH	367	
GEL	K NWRDPDQTDGL	GLSYLSSHIAN	416	3
VIL	Q KWTASNRTSGL	GKTHTVGSVAK	369	
ADS	G WDSSRW		715	
GEL	G WDDDYWSVDPL	-DRAMAELAA	782	
VIL	A WDPFKWSN TKS	YEDLKAESGN	734	6





Fig. 5E



Fig. 6

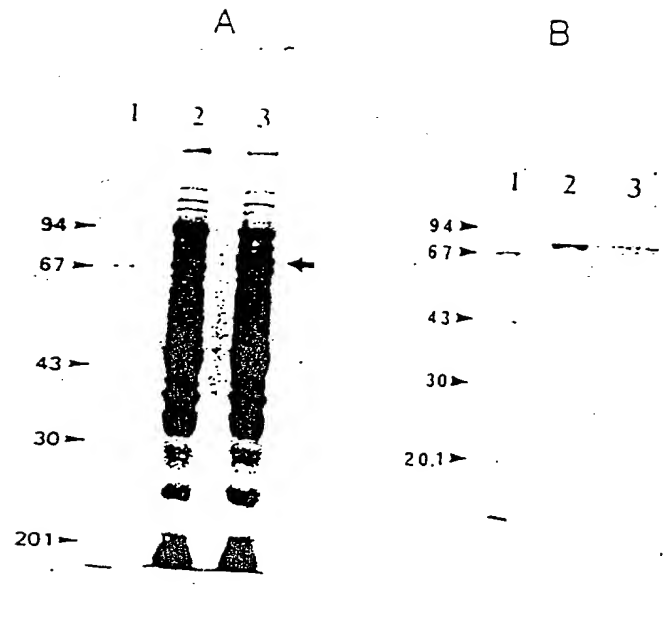
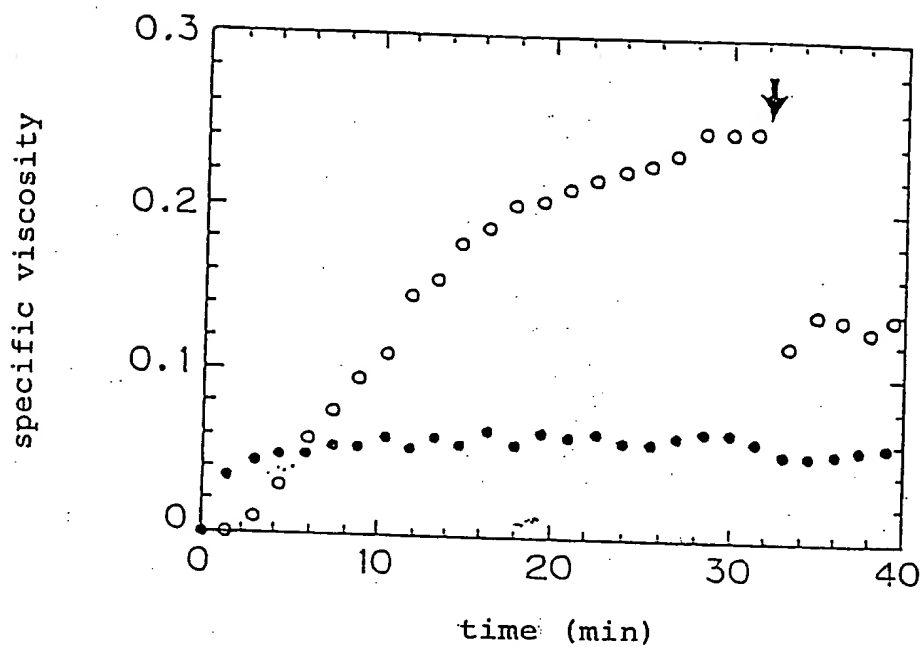


Fig. 7

A



B

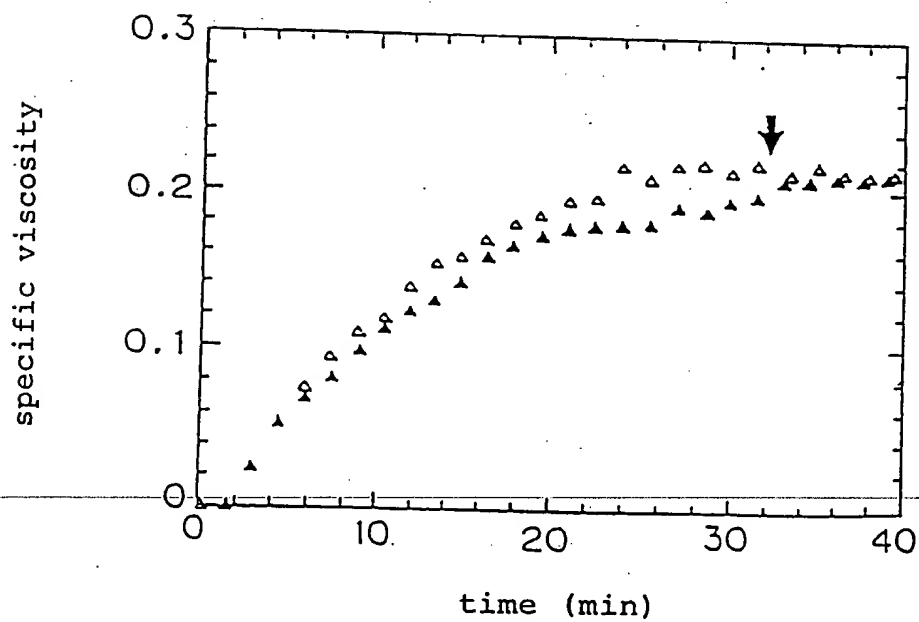
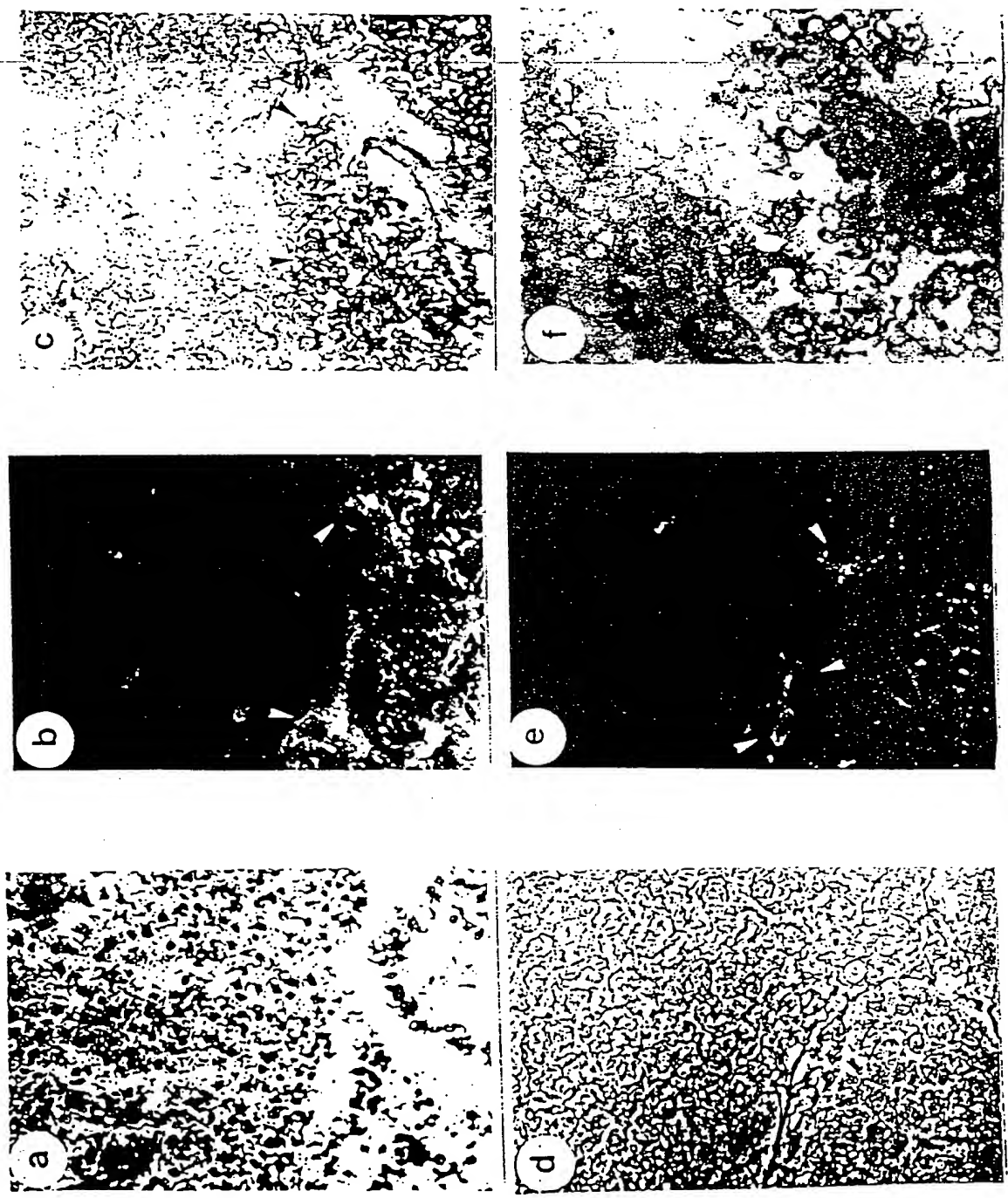


Fig. 8



## Fig. 9

1' MARELYHEEFARAGKQAGLQVWRIEXLELYPVPSAHGDFYVGDAYLVLHTAKTSRGFTY  
 .....  
 1" MAOGLYHEEFARAGKRAGLQVWRIEXLELYVPESAYGNFYVGDAYLVLHTTQASRGFTY  
 .....  
 61' HLHFWLGKECSQDESTAAAIFTVQMDOYLGGKPVQNRRELQGYESNDFVSYFKGGLKYKAG  
 .....  
 61" RLHFWLGKECTQDESTAAAIFTVQMDOYLGGKPVQNRRELQGYESTDFVGYFKGGLKYKAG  
 .....  
 121' GVASGLNHVLTNDLTAKRLHVKGRVVRATEVPLSWDSFNKGDCFIIDLGTETIYQWCGS  
 .....  
 121" GVASGLNHVLTNDLTACRLHVKGRVVRATEVPLSWDSFNKGDCFIIDLGTETIYQWCGS  
 .....  
 181' SCNKYERLKANQVATGIRYNERKGRSELIWEEGSEPSSELIKVLGEKPELPOGGD000II  
 .....  
 181" SCNKYERLKASQVAIGIRDNERKGRAQLIVVEEGSEPSSELTkVLGEKPKLRDGED000IK  
 .....  
 241' ADISNRKMAKLYMVSDASGSMRVTVVAEENPFMSMALLSEECFILDHGAAKQIFVWKGKD  
 .....  
 241" ADITNRKMAKLYMVSDASGSMKVS LVAEENPFMSMALLSEECFILDHGAAKQIFVWKGKD  
 .....  
 301' ANPQERKAAMKTAEEFLQQMNYSKNTQIQVLPEGGETPIFKQFFKDWRDKDQSDGFGKVV  
 .....  
 301" ANPQERKAAMKTAEEFLQQMNYSTNTQIQVLPEGGETPIFKQFFKDWRDRDQSDGFGKVV  
 .....  
 361' VTEKVAQIKQIPFDASKLHSSPQMAAQHNMVDDGSGKVEIWRVENNNGRIQVDQNSYGEFY  
 .....  
 361" VTEKVAHVQKIPFDASKLHSSPQMAAQHHVDDGSGKVQIWRVENNNGRVEIDRNSYGEFY  
 .....  
 421' GGDCYIILYTYPRGQIIYTWQGANATRDELTTSAFLTVQLDRSLGGQAVQIRVSQKPEV  
 .....  
 421" GGDCYIILYTYPRGQIIYTWQGANATRDELTTSAFLTVQLDRSLGGQAVQIRVSQKKEPA  
 .....  
 481' HLLSLFKDKPLIIYKNGTSKKGGQAPAPPTRLFQVRRNLASITRIVEVDVDANSLNSNDV  
 .....  
 481" HLLSLFKDKPLIIYKNGTSKKEGQAPAPP IRLFQVRRNLASITRIMEVDVDANSLNSNDV  
 .....  
 541' CVLKL PQNSGYIWVGKGASQEEKGAEYVASVLKCKTLRIQEGEPEEFWNSLGGKKDYQ  
 .....  
 541" FVLKL RQNNGYIWIGKGSTQEEKGAEYVASVLKCKTSTIQEGKEPEEFWNSLGGKKDYQ  
 .....  
 601' TSP LLETQAEDHPPRLYGCSNKTGRFVIEEIPGEFTQOOLAEDOVMLLD AWEQIFIWIGK  
 .....  
 601" TSP LLESQAEDHPPRLYGCSNKTGRFIEEVPGEFTQOOLAEDOVMLLD AWEQIFIWIGK  
 .....  
 661' DANEVEKKESLKS AKMYLETDP SGROKRTPIV IIKQGHEPPTFTGNFLGWDS SKW  
 .....  
 661" DANEVEKSESLS AKIYLETDP SGROKRTPIV IIKQGHEPPTFTGNFLGWDS SRW